

RE-RUN



1600

RAW SEQUENCE LISTING

DATE: 06/12/2003

PATENT APPLICATION: US/09/765,061D

TIME: 09:02:28

Input Set : A:\UTHou-16UTL 79-88.ST25.txt

Output Set: N:\CRF4\06122003\I765061D.raw

3 <110> APPLICANT: The Board of Regents of the University of Texas System
 5 <120> TITLE OF INVENTION: MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P CAUSE

LEBER

6 CONGENITAL AMAUROSIS (LCA4)

8 <130> FILE REFERENCE: 96606/16UTL

10 <140> CURRENT APPLICATION NUMBER: 09/765,061D

11 <141> CURRENT FILING DATE: 2001-01-17

13 <150> PRIOR APPLICATION NUMBER: 60/331362

14 <151> PRIOR FILING DATE: 2001-01-04

16 <160> NUMBER OF SEQ ID NOS: 10 additional sequences, Seq. Nos. 79-88

18 <170> SOFTWARE: PatentIn version 3.2

20 <210> SEQ ID NO: 79

21 <211> LENGTH: 34

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

26 <220> FEATURE:

27 <221> NAME/KEY: misc_feature

28 <222> LOCATION: (1)..(34)

29 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
 30 Residues 11-34 are the intronic sequence

32 <400> SEQUENCE: 79

33 cggatccgga gtgagtgggg ccctccggag caga

36 <210> SEQ ID NO: 80

37 <211> LENGTH: 35

38 <212> TYPE: DNA

39 <213> ORGANISM: Homo sapiens

42 <220> FEATURE:

43 <221> NAME/KEY: misc_feature

44 <222> LOCATION: (1)..(35)

45 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence
 46 and Residues 26-35 are the exonic sequence.

48 <400> SEQUENCE: 80

49 cagagtgcac cgtctcgggtg actaggtgat ctttc

52 <210> SEQ ID NO: 81

53 <211> LENGTH: 35

54 <212> TYPE: DNA

55 <213> ORGANISM: Homo sapiens

58 <220> FEATURE:

59 <221> NAME/KEY: misc_feature

60 <222> LOCATION: (1)..(35)

61 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
 62 Residues 11-35 are the intronic sequence

64 <400> SEQUENCE: 81

65 csacaccatc gtaagtaggc cctgcgcgcc tgtct

Does Not Comply
 Corrected Diskette Needed

invalid,
 per 1.825 of
 Sequence Rules.

"Any amendment to the
 paper copy of the Sequence Listing
 must be accompanied by a

34 substitute
 copy of the
 computer readable
 form... includes
 all previously
 submitted data...

35

35

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Input Set : A:\UTHou-16UTL 79-88.ST25.txt

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68 <210> SEQ ID NO: 82
69 <211> LENGTH: 35
70 <212> TYPE: DNA
71 <213> ORGANISM: Homo sapiens
74 <220> FEATURE:
75 <221> NAME/KEY: misc_feature
76 <222> LOCATION: (1)..(35)
77 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence
78     and Residues 26-35 are the exonic sequence.
80 <400> SEQUENCE: 82
81 gccatcctc cgtttatccc cacagcacac ggggg                                     35
84 <210> SEQ ID NO: 83
85 <211> LENGTH: 35
86 <212> TYPE: DNA
87 <213> ORGANISM: Homo sapiens
90 <220> FEATURE:
91 <221> NAME/KEY: misc_feature
92 <222> LOCATION: (1)..(35)
93 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
94     Residues 11-35 are the intronic sequence
96 <400> SEQUENCE: 83
97 gctgctgcag gtggggctgg ggttgccagg gctgg                                     35
100 <210> SEQ ID NO: 84
101 <211> LENGTH: 35
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
106 <220> FEATURE:
107 <221> NAME/KEY: misc_feature
108 <222> LOCATION: (1)..(35)
109 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
sequence
110     and Residues 26-35 are the exonic sequence.
112 <400> SEQUENCE: 84
113 cactgacctg cagctctggg gccaggttga tgccc                                     35
116 <210> SEQ ID NO: 85
117 <211> LENGTH: 35
118 <212> TYPE: DNA
119 <213> ORGANISM: Homo sapiens
122 <220> FEATURE:
123 <221> NAME/KEY: misc_feature
124 <222> LOCATION: (1)..(35)
125 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
126     Residues 11-35 are the intronic sequence
128 <400> SEQUENCE: 85
129 gcagaccaag gtcagaggcc gctggccacg ggggtg                                     35
132 <210> SEQ ID NO: 86
133 <211> LENGTH: 35
134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
138 <220> FEATURE:

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139 <221> NAME/KEY: misc_feature
140 <222> LOCATION: (1)..(35)
141 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
sequence
142      and Residues 26-35 are the exonic sequence.
144 <400> SEQUENCE: 86
145 catggctgac cttctccctg ggcaggagaa gccrt                      35
148 <210> SEQ ID NO: 87
149 <211> LENGTH: 35
150 <212> TYPE: DNA
151 <213> ORGANISM: Homo sapiens
154 <220> FEATURE:
155 <221> NAME/KEY: misc_feature
156 <222> LOCATION: (1)..(35)
157 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
158      Residues 11-35 are the intronic sequence
160 <400> SEQUENCE: 87
161 caccacccag gtgcgcgggg ctgcaggggc ggaca                      35
164 <210> SEQ ID NO: 88
165 <211> LENGTH: 35
166 <212> TYPE: DNA
167 <213> ORGANISM: Homo sapiens
170 <220> FEATURE:
171 <221> NAME/KEY: misc_feature
172 <222> LOCATION: (1)..(35)
173 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
sequence
174      and Residues 26-35 are the exonic sequence.
176 <400> SEQUENCE: 88
177 gctggatgct cctgctccc cacaggcatc gtgaa                      35

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/765,061D

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TIME: 09:02:29 - -

Input Set : A:\UTHou-16UTL 79-88.ST25.txt

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